

WEST Search History

32

DATE: Tuesday, February 27, 2007

<u>Hide?</u>	<u>Set Name Query</u>	<u>Hit Count</u>
<i>DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>		
<input type="checkbox"/>	L4 burioni.in. and (antibod\$ same (HCV or hepatitis adj C))	6
<input type="checkbox"/>	L3 l1 and (@ad<20020130 or @pd<20020130)	38
<input type="checkbox"/>	L2 L1 and e137	1
<input type="checkbox"/>	L1 neutraliz\$ near4 (antibod\$ or immunoglob\$) same (HCV or hepatitis adj C) with E2	77

END OF SEARCH HISTORY



Search for

Limits

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Field: Title/Abstract

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Search

Most Recent Queries

Time **Result**

#18 Search #16 AND #9 Field: Title/Abstract	09:20:01	41
#17 Search #16 AND #11 Field: Title/Abstract	09:18:23	146
#16 Related Articles for PubMed (Select 16250048)	09:18:06	284
#11 Related Articles for PubMed (Select 16501075)	09:18:00	601
#9 Search #8 AND (HCV[ti] or "hepatitis C"[ti]) Field: Title/Abstract	09:02:24	103
#8 Related Articles for PubMed (Select 12323399)	08:40:51	225
#6 Search (HCV[ti] or "hepatitis C"[ti]) AND (Fab or antibod\$ or immunoglob\$) Field: Title/Abstract	08:40:22	14
#5 Search (HCV[ti] or "hepatitis C"[ti]) AND (therap\$ or treat\$ or (passive AND vaccin\$)) Field: Title/Abstract	08:39:52	457
#4 Search (HCV or "hepatitis C") AND (therap\$ or treat\$ or (passive AND vaccin\$)) Field: Title/Abstract	08:39:41	620
#3 Search (HCV or "hepatitis C") AND (therap\$ or treat\$ or (passive AND vaccin\$))	08:39:29	15386
#1 Search (HCV or "hepatitis C") AND (therap\$ or treat\$) AND (immunoglob\$ or antibod\$ or (passive AND vaccin\$))	08:38:55	14

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Feb 21 2007 18:14:20

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BLASTP 2.2.15 [Oct-15-2006]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference:

Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005.

RID: 1172616815-29106-99909479111.BLASTQ3

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples
4,657,147 sequences; 1,607,774,624 total letters

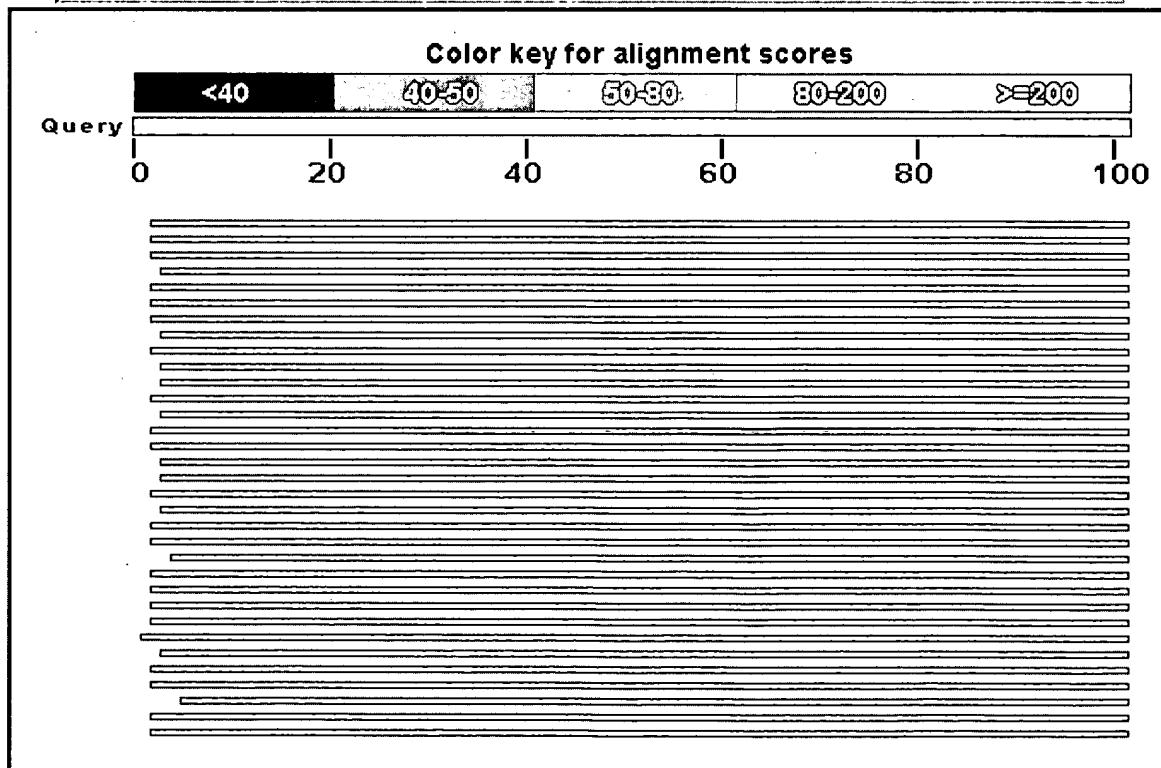
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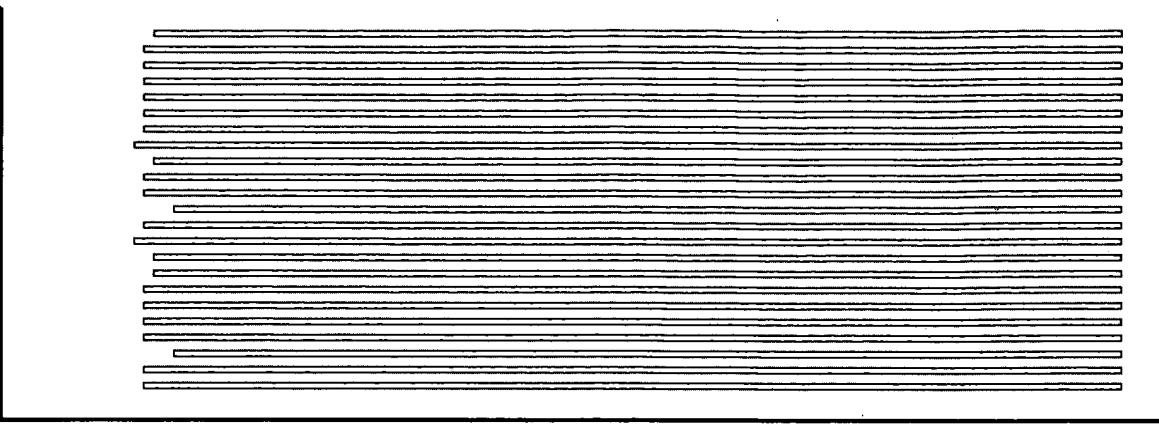
Query= SEQ 1D NO: 8

Length=102

Distribution of 101 Blast Hits on the Query Sequence

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Sequences producing significant alignments:

		Score (Bits)	E Value	
gi 12655526 emb CAC27614.11	immunoglobulin kappa chain variable	169	5e-41	
gi 21707884 gb AAH34141.11	IGKC protein [Homo sapiens]	167	2e-40	UG
gi 542883 pir S40336	Ig kappa chain V-J region - human >gi 4...	166	3e-40	
gi 21669487 dbj BAC01768.11	immunoglobulin kappa light chain VLJ	166	4e-40	U
gi 481992 pir S40334	Ig kappa chain - human	166	5e-40	
gi 441357 emb CAA51112.11	Ig kappa light chain (VJC) [Homo sapie	165	5e-40	U
gi 41388184 gb AAS01771.11	monoclonal IgM antibody light chain [165	6e-40	U
gi 4063659 gb AAC98364.11	scFV antibody V-region [synthetic cons	164	9e-40	
gi 58202720 gb AAW67411.11	rotavirus-specific intestinal-homi...	164	9e-40	U
gi 5690400 gb AAD47068.1 AF163306_1	anti-HLA-A2/A28 immunoglo...	164	1e-39	U
gi 4063657 gb AAC98363.11	scFV antibody V-region [synthetic cons	164	2e-39	
gi 77378175 gb ABA70812.11	immunoglobulin kappa light chain vari	164	2e-39	
gi 13171340 gb AAK13632.1 AF234256_1	immunoglobulin light chain	163	3e-39	U
gi 5360679 dbj BAA82105.11	anti-Entamoeba histolytica immunog...	163	3e-39	U
gi 114385548 gb ABI74032.11	immunoglobulin light chain variable	163	3e-39	
gi 51103393 gb AAT96422.11	immunoglobulin variable region VL kap	163	3e-39	U
gi 5081721 gb AAD39506.1 AF146408_1	antibody light chain variabl	163	3e-39	U
gi 49257007 gb AAH73791.11	IGKC protein [Homo sapiens]	162	3e-39	UG
gi 21669353 dbj BAC01701.11	immunoglobulin kappa light chain VLJ	162	3e-39	U
gi 567146 gb AAA52924.11	immunoglobulin gamma-chain, V region [H	162	4e-39	U
gi 7012707 gb AAF35179.11	immunoglobulin light chain variable re	162	5e-39	U
gi 306993 gb AAA20164.11	immunoglobulin light chain	162	6e-39	
gi 45501244 gb AAH67226.11	IGKC protein [Homo sapiens]	162	6e-39	UG
gi 63102969 gb AYY33390.11	anti-rabies virus immunoglobulin l...	162	6e-39	U
gi 11275318 dbj BAB18259.11	anti HBs antibody light-chain Fab fr	161	8e-39	U
gi 4063661 gb AAC98365.11	scFV antibody V-region [synthetic cons	161	8e-39	
gi 3046470 gb AAC13450.11	anti-Rh(D) antibody V kappa segment [s	161	8e-39	
gi 70798869 gb AAZ09144.11	immunoglobulin kappa light chain vari	161	9e-39	U
gi 63103079 gb AYY33445.11	anti-rabies virus immunoglobulin l...	161	1e-38	U
gi 542905 pir S40318	Ig kappa chain V region - human >gi 441...	161	1e-38	
gi 18307264 gb AAL65703.11	immunoglobulin light chain kappa vari	160	1e-38	
gi 12655530 emb CAC27616.11	immunoglobulin kappa chain variable	160	1e-38	
gi 732746 emb CAA84391.11	antibody, light chain variable regi...	160	1e-38	
gi 4063667 gb AAC98368.11	scFV antibody V-region [synthetic cons	160	1e-38	
gi 3644022 gb AAC43029.11	anti-mucin1 light chain variable regio	160	2e-38	U
gi 12655532 emb CAC27617.11	immunoglobulin kappa chain variable	160	2e-38	
gi 5081723 gb AAD39507.1 AF146409_1	antibody light chain variabl	160	2e-38	U

gi 93278678 pdb 2AJ3 A	Chain A, Crystal Structure Of A Cross...	160	2e-38	S
gi 47109384 emb CAG28673.1	anti-PLAP ScFv antibody [synthetic c	160	2e-38	
gi 63103033 gb AYY33422.1	anti-rabies virus immunoglobulin 1...	160	2e-38	U
gi 1514581 emb CAA65058.1	immunoglobulin kappa light chain [syn	160	2e-38	
gi 84797980 gb ABC66939.1	immunoglobulin light chain variabl...	160	2e-38	U
gi 21669293 dbj BAC01671.1	immunoglobulin kappa light chain VLJ	160	3e-38	
gi 5731263 gb AAD48839.1	single-chain Fv antibody SR19 [synthet	159	3e-38	
gi 58032607 gb AAW63086.1	anti-pneumococcal antibody 54B11 ligh	159	3e-38	
gi 12655528 emb CAC27615.1	immunoglobulin kappa chain variable	159	3e-38	
gi 33355929 gb AAQ16318.1	anti-human kappa light chain antib...	159	4e-38	
gi 29725718 gb AAO91639.1	anti-HLA-A2/A28 immunoglobulin lig...	159	4e-38	U
gi 58222496 gb AAW68880.1	anti-tetanus toxoid immunoglobulin...	159	4e-38	U
gi 13171342 gb AAK13633.1 AF234257_1	immunoglobulin light chain	159	4e-38	U
gi 49256425 gb AAH73764.1	IGKC protein [Homo sapiens]	159	4e-38	UG
gi 21669307 dbj BAC01678.1	immunoglobulin kappa light chain VLJ	159	4e-38	U
gi 567150 gb AAA52928.1	immunoglobulin gamma-chain, V region [H	159	5e-38	U
gi 4378190 gb AAD19430.1	immunoglobulin kappa light chain varia	159	5e-38	U
gi 186009 gb AAA62364.1	immunoglobulin kappa-chain VK-1 [Homo s	159	5e-38	U
gi 63101938 gb AAH95489.1	IGKC protein [Homo sapiens]	159	6e-38	UG
gi 4323882 gb AAD16580.1	immunoglobulin kappa light chain varia	159	6e-38	U
gi 55700563 emb CAH69219.1	anti-human-CD3-anti-human-HMWG.bi...	159	6e-38	
gi 21669363 dbj BAC01706.1	immunoglobulin kappa light chain VLJ	159	6e-38	U
gi 18092610 gb AAL59374.1	anti-cardiolipin immunoglobulin light	159	6e-38	
gi 114385751 gb ABI74133.1	immunoglobulin light chain variable	158	6e-38	
gi 77378173 gb ABA70811.1	immunoglobulin kappa light chain vari	158	6e-38	
gi 98956308 emb CAI99792.1	immunoglobulin kappa light chain var	158	7e-38	
gi 70798711 gb AAZ09065.1	immunoglobulin kappa light chain vari	158	7e-38	U
gi 21669297 dbj BAC01673.1	immunoglobulin kappa light chain VLJ	158	7e-38	U
gi 58222457 gb AAW68862.1	anti-tetanus toxoid immunoglobulin...	158	7e-38	U
gi 21998807 emb CAD43015.1	immunoglobulin kappa chain variable	158	7e-38	
gi 41388186 gb AAS01772.1	monoclonal IgM antibody light chain [158	7e-38	U
gi 109693151 gb ABG38368.1	immunoglobulin light chain variable	158	8e-38	
gi 114385626 gb ABI74071.1	immunoglobulin light chain variable	158	8e-38	
gi 542900 pir S40352	Ig kappa chain V-J-C region - human >gi...	158	9e-38	
gi 186006 gb AAA58934.1	Ig kappa V-region d	158	9e-38	
gi 70798670 gb AAZ09045.1	immunoglobulin kappa light chain vari	157	1e-37	U
gi 4379022 emb CAA77300.1	kappa immunoglobulin (subgroup V kapp	157	1e-37	G
gi 109240734 emb CAJ13477.1	immunoglobulin kappa chain variable	157	1e-37	U
gi 6179862 gb AAF05688.1	anti-phospholipid immunoglobulin li...	157	1e-37	U
gi 14573217 gb AAK67997.1	immunoglobulin light chain variable r	157	1e-37	U
gi 63103119 gb AYY33465.1	anti-rabies virus immunoglobulin 1...	157	1e-37	U
gi 109693101 gb ABG38344.1	immunoglobulin light chain variable	157	1e-37	
gi 84798214 gb ABC67056.1	immunoglobulin light chain variabl...	157	2e-37	U
gi 5731265 gb AAD48840.1	single-chain Fv antibody VE91 [synthet	157	2e-37	
gi 18025630 gb AAK94824.1	immunoglobulin light chain variable r	157	2e-37	U
gi 63103035 gb AYY33423.1	anti-rabies virus immunoglobulin 1...	157	2e-37	U
gi 4063665 gb AAC98367.1	scFV antibody V-region [synthetic cons	157	2e-37	
gi 6179868 gb AAF05691.1	anti-phospholipid immunoglobulin li...	157	2e-37	U
gi 14588867 emb CAC43029.1	immunoglobulin light chain variable	157	2e-37	
gi 58202724 gb AAW67413.1	rotavirus-specific intestinal-homolog...	157	2e-37	U
gi 12655492 emb CAC27598.1	immunoglobulin kappa chain variable	157	2e-37	
gi 33235610 dbj BAC80161.1	immunoglobulin kappa light chain [Ho	157	2e-37	U
gi 58222492 gb AAW68878.1	anti-tetanus toxoid immunoglobulin...	157	2e-37	U
gi 63103087 gb AYY33449.1	anti-rabies virus immunoglobulin 1...	157	2e-37	U

gi 482009 pir S40369	Ig kappa chain - human	>gi 441427 emb C...	156	2e-37
gi 75707211 gb ABA26069.1	immunoglobulin light chain variable r		156	2e-37
gi 63102911 gb AAY33361.1	anti-rabies virus immunoglobulin l...		156	2e-37
gi 21669365 dbj BAC01707.1	immunoglobulin kappa light chain VLJ		156	3e-37
gi 11275310 dbj BAB18255.1	anti TNF-alpha antibody light-chain		156	3e-37
gi 109693166 gb ABG38375.1	immunoglobulin light chain variab...		156	3e-37
gi 106669 pir S19674	Ig kappa chain V region (clone alpha-TE...		156	3e-37
gi 114385660 gb ABI74088.1	immunoglobulin light chain variable		156	3e-37
gi 90823197 gb ABE01099.1	anti-Rhesus D-specific antibody li...		156	3e-37

Alignments

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> gi|12655526|emb|CAC27614.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=106

Score = 169 bits (427), Expect = 5e-41, Method: Composition-based stats.
Identities = 93/100 (93%), Positives = 97/100 (97%), Gaps = 0/100 (0%)

Query 3	ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF	62
	+LTQSPSFLSASVGDRVTITCRASQGIS+YLAWYQQKPGKAPKLLIYAASTLQSGVPSRF	
Sbjct 2	QLTQSPSFLSASVGDRVTITCRASQGISYYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF	61
Query 63	SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT	102
	SGSGS TEFTLTI+ LQPEDFATYYCQ LN+YPWTFGQGT	
Sbjct 62	SGSGSGTEFTLTINSLQPEDFATYYCQQLNSYPWTFGQGT	101

> gi|21707884|gb|AAH34141.1| **UG** IGKC protein [Homo sapiens]
Length=236

Score = 167 bits (422), Expect = 2e-40, Method: Composition-based stats.
Identities = 90/100 (90%), Positives = 93/100 (93%), Gaps = 0/100 (0%)

Query 3	ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF	62
	+LTQSPSFLSASVGDRVTITCRASQGIS+YLAWYQQKPGKAP LLIYAASTLQSGVPSRF	
Sbjct 25	QLTQSPSFLSASVGDRVTITCRASQGISYYLAWYQQKPGKAPNLLIYAASTLQSGVPSRF	84
Query 63	SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT	102
	SGSGS TEFTLTIS LQPEDFATYYCQ LN+ P TFG GT	
Sbjct 85	SGSGSGTEFTLTISLQPEDFATYYCQQLNSPPTFGGGT	124

> gi|542883|pir||S40336 Ig kappa chain V-J region - human
gi|441361|emb|CAA51114.1| **U** Ig kappa light chain (VJ) [Homo sapiens]
Length=124

Score = 166 bits (420), Expect = 3e-40, Method: Composition-based stats.
Identities = 94/101 (93%), Positives = 97/101 (96%), Gaps = 1/101 (0%)

Query 3	ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF	62
	+LTQSPSFLSASVGDRVTITCRASQGIS+YLAWYQQKPGKAPKLLIYAASTLQSGVPSRF	
Sbjct 18	QLTQSPSFLSASVGDRVTITCRASQGISYYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF	77
Query 63	SGSGSWTEFTLTISRLQPEDFATYYCQHLNTY-PWTFGQGT	102
	SGSGS TEF+LTIS LQPEDFATYYCQ LNTY PWTFGQGT	
Sbjct 78	SGSGSGTEFSLTISLQPEDFATYYCQQLNTYPPWTFGQGT	118

> gi|21669487|dbj|BAC01768.1| **U** immunoglobulin kappa light chain VLJ region [Homo sapiens]

Length=264.

Score = 166 bits (420), Expect = 4e-40, Method: Composition-based stats.
Identities = 90/99 (90%), Positives = 93/99 (93%), Gaps = 0/99 (0%)

Query 4 LTQSPSFLSASVGDRVITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 63
LTQSPS LSASVGDRVITCRASQGIS+YLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS
Sbjct 26 LTQSPSSLSASVGDRVITCRASQGISSYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 85

Query 64 GSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
GSGS T+FTLTIS LQPEDFATYYCQ LN+YP TFG GT
Sbjct 86 GSGSGTDFTLTISLQPEDFATYYCQQLNSYPLTFGGGT 124

> gi|481992|pir||S40334 Ig kappa chain - human

Length=132

Score = 166 bits (419), Expect = 5e-40, Method: Composition-based stats.
Identities = 87/100 (87%), Positives = 94/100 (94%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
+LTQSPSFLSAS+GDRVITCRASQGI+YLAWYQQKPGKAPKLLIY ASTLQSGVPSRF
Sbjct 24 QLTQSPSFLSASIGDRVITCRASQGINSYLAWYQQKPGKAPKLLIYVASTLQSGVPSRF 83

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
SGSGS TEFTLTIS LQPEDFA+YYCQ N+YP+TFG GT
Sbjct 84 SGSGSGTEFTLTISLQPEDFASYYCQQFNSYPFTFGGGT 123

> gi|441357|emb|CAA51112.1| U Ig kappa light chain (VJC) [Homo sapiens]

Length=133

Score = 165 bits (418), Expect = 5e-40, Method: Composition-based stats.
Identities = 87/100 (87%), Positives = 94/100 (94%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
+LTQSPSFLSAS+GDRVITCRASQGI+YLAWYQQKPGKAPKLLIY ASTLQSGVPSRF
Sbjct 24 QLTQSPSFLSASIGDRVITCRASQGINSYLAWYQQKPGKAPKLLIYVASTLQSGVPSRF 83

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
SGSGS TEFTLTIS LQPEDFA+YYCQ N+YP+TFG GT
Sbjct 84 SGSGSGTEFTLTISLQPEDFASYYCQQFNSYPFTFGGGT 123

> gi|41388184|gb|AAS01771.1| U monoclonal IgM antibody light chain [Homo sapiens]

Length=236

Score = 165 bits (418), Expect = 6e-40, Method: Composition-based stats.
Identities = 87/100 (87%), Positives = 92/100 (92%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
++TQSPS LSASVGDRVITCRASQGISNYLAWYQQKPGK PKLLIYAASTLQSGVPSRF
Sbjct 25 QMTQSPSSLSASVGDRVITCRASQGISNYLAWYQQKPGKVKPCKLIYAASTLQSGVPSRF 84

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
SGSGS T+FTLTIS LQPED ATYYCQ N+ P+TFGQGT
Sbjct 85 SGSGSGTDFTLTISLQPEDVATYYCQKYNAPSFTFGQGT 124

> gi|4063659|gb|AAC98364.1| scFV antibody V-region [synthetic construct]

Length=232

Score = 164 bits (416), Expect = 9e-40, Method: Composition-based stats.
Identities = 85/99 (85%), Positives = 93/99 (93%), Gaps = 0/99 (0%)

Query 4 LTQSPSFLSASVGDRVITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 63
+TQSPS LSASVGDRVITCRASQGIS+LAWYQQKPGKAPKLL+Y AS+L+SGVPSRFS
Sbjct 128 MTQSPSTLSASVGDRVITCRASQGISSWLAWYQQKPGKAPKLLMYEASSLESGVPSRFS 187

Query 64 GSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
GSGS TEFTLTIS LQP+DFA YYCQH NTYP+TFGQGT
Sbjct 188 GSGSGTEFTLTISLQPDDFAAYYCQHYNTYPYTFGQGT 226

> gi|58202720|gb|AAW67411.1| U rotavirus-specific intestinal-homing antibody light chain variable region [Homo sapiens]
Length=109

Score = 164 bits (416), Expect = 9e-40, Method: Composition-based stats.
Identities = 91/100 (91%), Positives = 95/100 (95%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
++TQSPSFLSASVGDRVITCRASQGIS+YLAWYQQKPGKAPKLLIYAASTLQSGVPSRF
Sbjct 5 QVTQSPSFLSASVGDRVITCRASQGISSYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 64

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
SGSGS TEFTLTIS LQPEDFATYYCQ LN+YP TFG GT
Sbjct 65 SGSGSGTEFTLTISLQPEDFATYYCQQLNSYPLTFGGGT 104

> gi|5690400|gb|AAD47068.1|AF163306_1 U anti-HLA-A2/A28 immunoglobulin light chain variable region [Homo sapiens]
Length=108

Score = 164 bits (416), Expect = 1e-39, Method: Composition-based stats.
Identities = 88/99 (88%), Positives = 93/99 (93%), Gaps = 0/99 (0%)

Query 4 LTQSPSFLSASVGDRVITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 63
+TQSPSFLSASVGDRVITCRASQ GI+NYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS
Sbjct 4 MTQSPSFLSASVGDRVITCRASHGINNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 63

Query 64 GSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
GSGS TEFTLTIS LQPEDFATYYCQ ++YP TFG+GT
Sbjct 64 GSGSGTEFTLTISLQPEDFATYYCQYDSYPPTFGRGT 102

> gi|4063657|gb|AAC98363.1| scFv antibody V-region [synthetic construct]
Length=232

Score = 164 bits (414), Expect = 2e-39, Method: Composition-based stats.
Identities = 84/99 (84%), Positives = 92/99 (92%), Gaps = 0/99 (0%)

Query 4 LTQSPSFLSASVGDRVITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 63
+TQSPS LSASVGDRVITCRASQ IS++LAWYQQKPGKAPKLL+Y AS+L+SGVPSRFS
Sbjct 128 MTQSPSTLSASVGDRVITCRASQSISSWLAWYQQKPGKAPKLLMYEASSLESGVPSRFS 187

Query 64 GSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
GSGS TEFTLTIS LQP+DFA YYCQH NTYP+TFGQGT
Sbjct 188 GSGSGTEFTLTISLQPDDFAAYYCQHYNTYPYTFGQGT 226

> gi|77378175|gb|ABA70812.1| immunoglobulin kappa light chain variable region [Homo sapiens]
Length=128

Score = 164 bits (414), Expect = 2e-39, Method: Composition-based stats.
Identities = 90/101 (89%), Positives = 91/101 (90%), Gaps = 1/101 (0%)

Query 3 ELTQSPSFLSASVGDRVITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62

Sbjct 14 +LT SPSFLSASVGDRVTITCRASQGI NYLAWYQQKPGKAPKLLIYAASTL SGVPSRF
QLTPSPSFLSASVGDRVTITCRASQGI NYLAWYQQKPGKAPKLLIYAASTL HSGVPSRF 73

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWT-FGQGT 102
SGSGS TEFTLTIS LQPEDFATYYCQ LNTYP FG GT

Sbjct 74 SGSGSGTEFTLTISLQPEDFATYYCQQLNTYPGVIFGPGT 114

> gi|13171340|gb|AAK13632.1|AF234256_1 **U** immunoglobulin light chain variable region [Homo sapiens]
Length=107

Score = 163 bits (412), Expect = 3e-39, Method: Composition-based stats.
Identities = 88/99 (88%), Positives = 92/99 (92%), Gaps = 0/99 (0%)

Query 4 LTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 63
+TQSPSFLSASVGDRVTITCRASQGISNYLAWYQQ+PGKAPKLLIYAASTLQ+GVPSRFS

Sbjct 4 MTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQRPGKAPKLLIYAASTLQTVPSRFS 63

Query 64 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102

SGSGS TEFTLTIS LQPEDFATY+CQ L YP TFG GT

Sbjct 64 SGSGSGTEFTLTISLQPEDFATYFCQQLGGYPLTFGGGT 102

> gi|5360679|dbj|BAA82105.1| **U** anti-Entamoeba histolytica immunoglobulin kappa light chain [Homo sapiens]

Length=215

Score = 163 bits (412), Expect = 3e-39, Method: Composition-based stats.
Identities = 90/101 (89%), Positives = 94/101 (93%), Gaps = 1/101 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 62
++TQSPSFLSASVGDRVTITCRASQGIS+YLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS

Sbjct 3 QMTQSPSFLSASVGDRVTITCRASQGISYYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 62

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTY-PWTFGQGT 102

SGSGS TEFTLTIS LQPEDFATYYCQ LN+Y TFG GT

Sbjct 63 SGSGSGTEFTLTISLQPEDFATYYCQQLNSYLALTFFGGT 103

> gi|114385548|gb|ABI74032.1| immunoglobulin light chain variable region [Homo sapiens]
Length=110

Score = 163 bits (412), Expect = 3e-39, Method: Composition-based stats.
Identities = 89/100 (89%), Positives = 94/100 (94%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 62

ELTQSPSFLSASVGDRVTITCRASQGIS+YLAWYQQKPGKAPKLLIYAAS+LQSGVPSRFS

Sbjct 3 ELTQSPSFLSASVGDRVTITCRASQGISYYLAWYQQKPGKAPKLLIYAASSLQSGVPSRFS 62

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102

SGSGS T+FTLTIS LQPEDFATYYCQ N++P TFG GT

Sbjct 63 SGSGSGTDFTLTISLQPEDFATYYCQQANSFPLTFGGGT 102

> gi|51103393|gb|AAT96422.1| **U** immunoglobulin variable region VL kappa domain [Homo sapiens]
Length=107

Score = 163 bits (412), Expect = 3e-39, Method: Composition-based stats.
Identities = 90/99 (90%), Positives = 93/99 (93%), Gaps = 0/99 (0%)

Query 4 LTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 63

LTQSPSFLSASVGDRVTITCRASQGIS YLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS

Sbjct 4 LTQSPSFLSASVGDRVTITCRASQGISYYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 63

Query 64 . GSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
GSGS T+FTLTIS LQPEDFATYYCQ N+ P+TFGQGT
Sbjct 64 GSGSGTDFTLTISTLQPEDFATYYCQQFNSNPYTFGQGT 102

>gi|5081721|gb|AAD39506.1|AF146408_1 **V** antibody light chain variable region [Homo sapiens]
Length=108

Score = 163 bits (412), Expect = 3e-39, Method: Composition-based stats.
Identities = 88/99 (88%), Positives = 91/99 (91%), Gaps = 0/99 (0%)

Query 4 LTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 63
+TQSPSFLSA VGDR+TITCRASQGIS YLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS
Sbjct 4 MTQSPSFLSAFVGDRITITCRASQGISGYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 63

Query 64 GSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
GSGS TEFITLTIS LQPED ATYYCQ N+ PWTFGQGT
Sbjct 64 GSGSGTEFTLTISGLQPEDFATYYCQKYNSAPWTFGQGT 102

>gi|49257007|gb|AAH73791.1| **VG** IGKC protein [Homo sapiens]
Length=236

Score = 162 bits (411), Expect = 3e-39, Method: Composition-based stats.
Identities = 86/100 (86%), Positives = 90/100 (90%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
++TQSPS LSASVGDRVTITCRASQGISN L WYQQKPGKAPKLLIYAAS+LQSGVPSRF
Sbjct 25 QMTQSPSSLSASVGDRVTITCRASQGISNDLGWYQQKPGKAPKLLIYAASSLQSGVPSRF 84

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
SGSGS T+FTLTIS LQPEDFATYYC YPWTFGQGT
Sbjct 85 SGSGSGTDFTLTISSLQPEDFATYYCLQDYNYPWTFGQGT 124

>gi|21669353|dbj|BAC01701.1| **V** immunoglobulin kappa light chain VLJ region [Homo sapiens]
Length=269

Score = 162 bits (411), Expect = 3e-39, Method: Composition-based stats.
Identities = 84/99 (84%), Positives = 88/99 (88%), Gaps = 0/99 (0%)

Query 4 LTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 63
+TQSPS LSASVGDRVT TCRAS+GI N L WYQQKPGKAP+ LIYAASTLQSGVPSRFS
Sbjct 26 MTQSPSSLSASVGDRVTFTCRASRGIRNDLGWYQQKPGKAPERLIYAASTLQSGVPSRF 85

Query 64 GSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
GSGS TEFITLTIS LQPEDFATYYC N+YPWTFGQGT
Sbjct 86 GSGSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGT 124

>gi|567146|gb|AAA52924.1| **V** immunoglobulin gamma-chain, V region [Homo sapiens]
Length=149

Score = 162 bits (411), Expect = 4e-39, Method: Composition-based stats.
Identities = 89/100 (89%), Positives = 91/100 (91%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
ELTQSPS LSASVGDRVTITCRASQGISNYLAWYQQKPGK PKLLIYAASTLQSGVPSRF
Sbjct 1 ELTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRF 60

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
SGSGS T+FTLTIS LQPED ATYYCQ N+ P TFGQGT
Sbjct 61 SGSGSGTDFTLTISSLQPEDFATYYCQKYNSAPRTFGQGT 100

> gi|7012707|gb|AAF35179.1| **U** immunoglobulin light chain variable region [Homo sapiens]
Length=107

Score = 162 bits (410), Expect = 5e-39, Method: Composition-based stats.
Identities = 88/100 (88%), Positives = 92/100 (92%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
++TQSPS LSASVGDRVTITCRASQGI NYLAW+QQKPGKAPK LIYAAS LQSGVPSRF
Sbjct 3 QMTQSPSFLSASVGDRVTITCRASQGIRNYLAWFQQKPGKAPKSLIYAASNLLQSGVPSRF 62

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
SGSGS T+FTLTIS LQPEDFATYYCQ NTYPWTFGQGT
Sbjct 63 SGSGSGTDFTLTISSLQPEDFATYYCQHQHNTYPWTFGQGT 102

> gi|306993|gb|AAA20164.1| immunoglobulin light chain
Length=104

Score = 162 bits (409), Expect = 6e-39, Method: Composition-based stats.
Identities = 89/98 (90%), Positives = 95/98 (96%), Gaps = 0/98 (0%)

Query 5 TQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFSG 64
TQSPSFLSASVGDRVT+TCRASQGIS+YLAWEQQKPGKAPKLLIYAASTL+SGVP+RFSG
Sbjct 1 TQSPSFLSASVGDRVTTCRASQGISSYLAWEQQKPGKAPKLLIYAASTLESGVPTRFSG 60

Query 65 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
SGS TEFTLTIS LQPEDFATYYCQ LN+YP+TFGQGT
Sbjct 61 SGSGTEFTLTISLQPEDFATYYCQQLNSYPFTFGQGT 98

> gi|45501244|gb|AAH67226.1| **UG** IGKC protein [Homo sapiens]
Length=236

Score = 162 bits (409), Expect = 6e-39, Method: Composition-based stats.
Identities = 84/100 (84%), Positives = 88/100 (88%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
+LTQSPSFLSA+VGDRV+ITCRASQ IS YLAWEQ K GKAPKLLIY ASTLQSGVPSRF
Sbjct 25 QLTQSPSFLSAAVGDRVSITCRASQDISKYLAWEQHKIGKAPKLLIYGASTLQSGVPSRF 84

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
SGSGS TEFTLTIS LQPED ATYYCQ LN YP TFG GT
Sbjct 85 SGSGSGTEFTLTINSLQPEDLATYYCQQLNNYPLTFGGGT 124

> gi|63102969|gb|AAY33390.1| **U** anti-rabies virus immunoglobulin light chain variable region [Homo sapiens]
Length=107

Score = 162 bits (409), Expect = 6e-39, Method: Composition-based stats.
Identities = 90/100 (90%), Positives = 95/100 (95%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
++TQSPSFLSASVGDRVTITCRASQGIS+YLAWEQQKPGKAPKLLIYAASTLQSGVPSRF
Sbjct 3 QMTQSPSFLSASVGDRVTITCRASQGIISSYLAWEQQKPGKAPKLLIYAASTLQSGVPSRF 62

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
SGSGS TEFTLTIS LQPEDFATY CQ L++YP TFGQGT
Sbjct 63 SGSGSGTEFTLTISLQPEDFATYSCQQLDSYPITFGQGT 102

> gi|11275318|dbj|BAB18259.1| **U** anti HBs antibody light-chain Fab fragment [Homo sapiens]
Length=214

Score = 161 bits (408), Expect = 8e-39, Method: Composition-based stats.
Identities = 83/100 (83%), Positives = 88/100 (88%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
ELTQSPS ++ASVGDRVTITCRASQGI NYL W+QQKPGK PK LIYAAS+LQSGVPSRF
Sbjct 3 ELTQSPSAMAASVGDRVTITCRASQGIGNYLWQFQQKPGKVKRLIYAASSLQSGVPSRF 62

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHNTYPWTFGQGT 102
SGSGS TEFTLTIS LQPEDFATYYC H N YP +FG GT
Sbjct 63 SGSGSGTEFTLTISLQPEDFATYYCLHHNNYPLSFGGGT 102

> gi|4063661|gb|AAC98365.1| scFV antibody V-region [synthetic construct]
Length=232

Score = 161 bits (408), Expect = 8e-39, Method: Composition-based stats.
Identities = 84/100 (84%), Positives = 93/100 (93%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
++TQSPS LSASVGDRVTITCRASQ IS++LAWYQQKPGKAPKLL+Y AS+L+SGVPSRF
Sbjct 127 QMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLMYEASSLESGVPSRF 186

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHNTYPWTFGQGT 102
SGSGS TEFTLTIS LQP+DFA YYCQH NTYP+TFGQGT
Sbjct 187 SGSGSGTEFTLTISLQPDDFAAYYCQHYNTYPWTFGQGT 226

> gi|3046470|gb|AAC13450.1| anti-Rh(D) antibody V kappa segment [synthetic construct]
Length=107

Score = 161 bits (408), Expect = 8e-39, Method: Composition-based stats.
Identities = 91/102 (89%), Positives = 96/102 (94%), Gaps = 1/102 (0%)

Query 2 AELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSR 61
AELTQSPSFLSASVGDRVTITCRASQGI++YLAWYQQKPGKAPKLLIYAASTLQSGVPSR
Sbjct 1 AELTQSPSFLSASVGDRVTITCRASQGISYLAWYQQKPGKAPKLLIYAASTLQSGVPSR 60

Query 62 FSGSGSWTEFTLTISRLQPEDFATYYCQHNTY-PWTFGQGT 102
FSGSGS TEFTLTIS LQP+DFAATYYCQ LN Y P+TFG GT
Sbjct 61 FSGSGSGTEFTLTIASLQPDDFATYYCQQLNNYPPFTFGPGT 102

> gi|70798869|gb|AAZ09144.1| U immunoglobulin kappa light chain variable region [Homo sapiens]
Length=109

Score = 161 bits (408), Expect = 9e-39, Method: Composition-based stats.
Identities = 89/99 (89%), Positives = 93/99 (93%), Gaps = 0/99 (0%)

Query 4 LTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 63
LTQSPSFLSASVGDRVTITCRASQGIS+YLAW+QQ PGKAPKLLIYAASTLQSGVPSRFS
Sbjct 1 LTQSPSFLSASVGDRVTITCRASQGISYYLAWFQQNPGKAPKLLIYAASTLQSGVPSRFS 60

Query 64 GSGSWTEFTLTISRLQPEDFATYYCQHNTYPWTFGQGT 102
GSGS TEFTLTIS LQPEDFATYYCQ +N+YP TFG GT
Sbjct 61 GSGSGTEFTLTISLQPEDFATYYCQQVNSYPLTFGGGT 99

> gi|63103079|gb|AAY33445.1| U anti-rabies virus immunoglobulin light chain variable region
[Homo sapiens]
Length=107

Score = 161 bits (407), Expect = 1e-38, Method: Composition-based stats.
Identities = 89/100 (89%), Positives = 95/100 (95%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAIASTLQSGVPSRF 62
+LTQSPS LSASVGDRVTITCRASQGI+YLAQYQQ+PGKAPKLLIYAIASTLQSGVPSRF
Sbjct 3 QLTQSPSTLSASVGDRVTITCRASQGINSYLAWYQQEPGKAPKLLIYAIASTLQSGVPSRF 62

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
SGSGS TEFTLTIS LQPEDFATYYCQ LN+YP+TFG GT
Sbjct 63 SGSGSGTEFTLTISLQPEDFATYYCQQLNSYPFTFGPGT 102

> gi|542905|pir|S40318 Ig kappa chain V region - human
gi|441325|emb|CAA51096.1| Ig kappa light chain (VJ) [Homo sapiens]
Length=124

Score = 161 bits (407), Expect = 1e-38, Method: Composition-based stats.
Identities = 87/100 (87%), Positives = 94/100 (94%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAIASTLQSGVPSRF 62
+LTQSPSFLSASVGDRVTITCRASQGIS+YLAQYQQ+G+APK+LIYAIASTLQSGVPSRF
Sbjct 19 QLTQSPSFLSASVGDRVTITCRASQGIGSSYLAWYQQKVGEAPKVLIIYAIASTLQSGVPSRF 78

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
SGSGS TEFTLTIS LQPEDFATYYCQ +N+YP TFGQGT
Sbjct 79 SGSGSGTEFSLTISLQPEDFATYYCHQVNSYPFTFGQGT 118

> gi|18307264|gb|AAL65703.1| immunoglobulin light chain kappa variable region [Homo sapiens]
Length=102

Score = 160 bits (406), Expect = 1e-38, Method: Composition-based stats.
Identities = 90/97 (92%), Positives = 92/97 (94%), Gaps = 0/97 (0%)

Query 6 QSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAIASTLQSGVPSRSGS 65
QSPSFLSASVGDRVTITCRASQGIS+YLAQYQQKPGKAPKLLIYAIASTLQSGVPSRSGS
Sbjct 1 QSPSFLSASVGDRVTITCRASQGIGSSYLAWYQQKPGKAPKLLIYAIASTLQSGVPSRSGS 60

Query 66 GSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
GS TEFTLTIS LQPEDFATYYCQ LN+YP TFGQGT
Sbjct 61 GSGTEFTLTISLQPEDFATYYCQQLNSYPLAFGQGT 97

> gi|12655530|emb|CAC27616.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=103

Score = 160 bits (406), Expect = 1e-38, Method: Composition-based stats.
Identities = 90/100 (90%), Positives = 94/100 (94%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAIASTLQSGVPSRF 62
+LTQSPSFLSAS+ DRVTITCRASQGIS+YLAQYQQKPGKAPKLLIYAIASTLQSGVPSRF
Sbjct 2 QLTQSPSFLSASIRDRVTITCRASQGIGSSYLAWYQQKPGKAPKLLIYAIASTLQSGVPSRF 61

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
SGSGS TEFTLTIS LQPEDFATYYCQ LN+YP TFGQGT
Sbjct 62 SGSGSGTEFTLTISLQPEDFATYYCQQLNSYPLAFGQGT 101

> gi|732746|emb|CAA84391.1| antibody, light chain variable region to HIV1 gp41 [Homo sapiens]
Length=115

Score = 160 bits (406), Expect = 1e-38, Method: Composition-based stats.
Identities = 89/102 (87%), Positives = 95/102 (93%), Gaps = 2/102 (1%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAIASTLQSGVPSRF 62
+LTQSPSFLSASVGDRVTITCRASQGIS+YLAQYQQKPGKAPKLLIYAIASTLQSGVPSRF

Sbjct 8 QLTQSPSFLSASVGDRVTITCRASQGIGSSYLAWYQQKPGKAPKLLIYAASLTLQSGVPSRF 67

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYP--WTFQQGT 102

SGSGS +FTLTIS LQPEDFATYYCQ LN++P +TFG GT

Sbjct 68 SGSGSGPDTLTISLQPEDFATYYCQQLNSFPRVFTFGPGT 109

> gi|4063667|gb|AAC98368.1| scFv antibody V-region [synthetic construct]

Length=228

Score = 160 bits (406), Expect = 1e-38, Method: Composition-based stats.

Identities = 87/99 (87%), Positives = 90/99 (90%), Gaps = 0/99 (0%)

Query 4 LTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASLTLQSGVPSRF 63

LTQSPSFLSASVGDRVTITCRAS GISNYLAWYQ KPGKAPKLLIYAASLTLQ+GVPS FS

Sbjct 124 LTQSPSFLSASVGDRVTITCRASHGISNYLAWYQHKPGKAPKLLIYAASLTLQNGVPSTFS 183

Query 64 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFQQGT 102

SGSGS TEFTLTIS LQP+DFATYYCQ L +YP TFG GT

Sbjct 184 GSGSGTEFTLTISLQPDDFATYYCQQLISYPLTFGGGT 222

> gi|3644022|gb|AAC43029.1| U anti-mucin1 light chain variable region [Homo sapiens]

Length=107

Score = 160 bits (405), Expect = 2e-38, Method: Composition-based stats.

Identities = 88/100 (88%), Positives = 93/100 (93%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASLTLQSGVPSRF 62

++TQSPSFLSASVGDRVTITCRASQGIS+ AWYQQKPGKAPKLLIYAASLTLQSGVPSRF

Sbjct 3 QMTQSPSFLSASVGDRVTITCRASQGISNNFAWYQQKPGKAPKLLIYAASLTLQSGVPSRF 62

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFQQGT 102

SGSGS TEFTLTIS LQPEDFATYYCQ LN++P TFGQGT

Sbjct 63 SGSGFGTEFTLTISLQPEDFATYYCQQLNSFPRTFGQGT 102

> gi|12655532|emb|CAC27617.1| immunoglobulin kappa chain variable region [Homo sapiens]

Length=104

Score = 160 bits (405), Expect = 2e-38, Method: Composition-based stats.

Identities = 93/101 (92%), Positives = 95/101 (94%), Gaps = 1/101 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASLTLQSGVPSRF 62

+LTQSPSFLSASVGDRVTITCRASQGIS+YLAWYQQKPGKAP LLIYAASLTLQSGVPSRF

Sbjct 2 QLTQSPSFLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPNLLIYAASLTLQSGVPSRF 61

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPW-TFGQGT 102

SGSGS TEFTLTIS LQPEDFATYYCQHLN YP TFGQGT

Sbjct 62 SGSGSGTEFTLTISLQPEDFATYYCQHLNGYPPNTFGQGT 102

> gi|5081723|gb|AAD39507.1|AF146409_1 U antibody light chain variable region [Homo sapiens]

Length=108

Score = 160 bits (405), Expect = 2e-38, Method: Composition-based stats.

Identities = 87/100 (87%), Positives = 93/100 (93%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASLTLQSGVPSRF 62

++TQSPSFLSASVGDRVTITCRASQ I+++AWYQQKPGKAPKLLIYAAS LQSGVPSRF

Sbjct 3 QMTQSPSFLSASVGDRVTITCRASQHINSLAWYQQKPGKAPKLLIYAASRLQSGVPSRF 62

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFQQGT 102

SGSGS TEFTLTIS LQPEDFATYYCQ LN+YP TFG GT

Sbjct 63 . SGSGSGTEFTLTISLQPEDFATYYCQQLNSYPLTFGGGT 102

> gi|93278678|pdb|2AJ3|A **S** Chain A, Crystal Structure Of A Cross-Reactive Hiv-1 Neutralizing Cd4-Binding Site Antibody Fab M18

gi|93278680|pdb|2AJ3|C **S** Chain C, Crystal Structure Of A Cross-Reactive Hiv-1 Neutralizing Cd4-Binding Site Antibody Fab M18

gi|93278682|pdb|2AJ3|E **S** Chain E, Crystal Structure Of A Cross-Reactive Hiv-1 Neutralizing Cd4-Binding Site Antibody Fab M18

Length=213

Score = 160 bits (405), Expect = 2e-38, Method: Composition-based stats.
Identities = 83/100 (83%), Positives = 90/100 (90%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
++TQSPSFLSASVGDRV+ITCRASQ I +LAWYQ PG APKLL+Y+ASTLQSGVPSRF

Sbjct 2 QMTQSPSFLSASVGDRVSIITCRASQDIQKFLAWYQLTPGDAPKLLMYSASTLQSGVPSRF 61

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
SGSGS TEFTLTIS LQPEDFATYYCQHL YP+TFGQGT

Sbjct 62 SGSGSGTEFTLTISGLQPEDFATYYCQHLKRYPYTFGQGT 101

> gi|47109384|emb|CAG28673.1| anti-PLAP ScFv antibody [synthetic construct]

Length=246

Score = 160 bits (405), Expect = 2e-38, Method: Composition-based stats.
Identities = 89/100 (89%), Positives = 91/100 (91%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
ELTQSPS LSASVGDRVITCRASQGISNYLAWYQQKPGK PKLLIYAASTLQSGVPSRF

Sbjct 132 ELTQSPSSLSASVGDRVITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRF 191

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
SGSGS T+FTLTIS LQPED ATYYCQ N+ P TFGQGT

Sbjct 192 SGSGSGTDFTLTISLQPEDVATYYCQKYNAPRTFGQGT 231

> gi|63103033|gb|AAY33422.1| **U** anti-rabies virus immunoglobulin light chain variable region [Homo sapiens]

Length=107

Score = 160 bits (404), Expect = 2e-38, Method: Composition-based stats.
Identities = 89/100 (89%), Positives = 94/100 (94%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
+LTQSPS LSASVGDRVITCRASQGIS++LAWYQQKPGKAPKLLIYAAS+LQSGVPSRF

Sbjct 3 QLTQSPSSLSASVGDRVITCRASQGISSSHAWYQQKPGKAPKLLIYAASSLQSGVPSRF 62

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
SGSGS TEFTLTIS LQPEDFATYYCQ N+YP TFGQGT

Sbjct 63 SGSGSGTEFTLTISLQPEDFATYYCQQFNSYPITFGQGT 102

> gi|1514581|emb|CAA65058.1| immunoglobulin kappa light chain [synthetic construct]

Length=234

Score = 160 bits (404), Expect = 2e-38, Method: Composition-based stats.
Identities = 85/101 (84%), Positives = 95/101 (94%), Gaps = 0/101 (0%)

Query 2 AELETQSPSFLSASVGDRVITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSR 61
AELETQSPS +SASVGDRVITCRASQGIS++LAWYQQKPGKAPKLLIY+AS+LQSGVPSR

Sbjct 22 AELETQSPSSVSASVGDRVITCRASQGISWLAWYQQKPGKAPKLLIYSASSLQSGVPSR 81

Query 62 FSGSGSWTEFTLTISRLQPEDFATYYCQHQLNTYPWTFGQGT 102
FSGSGS T+F+LTIS LQPED ATYYCQ N++P+TFGQGT
Sbjct 82 FSGSGSGTDFSLTISSLQPEDSATYYCQQANSFPYTFGQGT 122

>gi|84797980|gb|ABC66939.1| **U** immunoglobulin light chain variable region EM5-PPS-14-K1-1 [Homo sapiens]
Length=119

Score = 160 bits (404), Expect = 2e-38, Method: Composition-based stats.
Identities = 89/99 (89%), Positives = 94/99 (94%), Gaps = 1/99 (1%)

Query 4 LTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 63
+TQSPSFLSASVGD+VTITCRASQGIS+YLAWSYQQKPGKAPKLLIYAASTLQSGVPSRFS
Sbjct 6 MTQSPSFLSASVGDKVTITCRASQGISSYLAWSYQQKPGKAPKLLIYAASTLQSGVPSRFS 65

Query 64 GSGSWTEFTLTISRLQPEDFATYYCQHQLNTYPWTFGQGT 102
GSGS TEFTLTIS LQPEDFATYYCQ LN+YP+ FG GT
Sbjct 66 GSGSGTEFTLTISLQPEDFATYYCQQLNNSYPF-FGGGT 103

>gi|21669293|dbj|BAC01671.1| **U** immunoglobulin kappa light chain VLJ region [Homo sapiens]
Length=271

Score = 160 bits (404), Expect = 3e-38, Method: Composition-based stats.
Identities = 84/100 (84%), Positives = 93/100 (93%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
++TQSPS LSASVGDRVTITCRASQ +++YL WYQQKPGKAPKLLIYAAS+LQSGVPSRF
Sbjct 25 QMTQSPSSLSASVGDRVTITCRASQSVTSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF 84

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHQLNTYPWTFGQGT 102
SGSGS TEFTLTIS LQP+DFATYYCQ N+YP+TFGQGT
Sbjct 85 SGSGSGTEFTLTISLQPDFATYYCQQYNSYPYTFGQGT 124

>gi|5731263|gb|AAD48839.1| single-chain Fv antibody SR19 [synthetic construct]
Length=248

Score = 159 bits (403), Expect = 3e-38, Method: Composition-based stats.
Identities = 84/100 (84%), Positives = 92/100 (92%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
++TQSPS LSASVGD+VTITCRASQ IS+YL WYQQKPGKAPKLLIYAAS+LQSGVPSRF
Sbjct 143 QMTQSPSSLSASVGDKVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF 202

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHQLNTYPWTFGQGT 102
SGSGS T+FTLTIS LQP+DFATYYCQ N+Y WTFGQGT
Sbjct 203 SGSGSGTDFLTISLQPDFATYYCQQYNSWTFGQGT 242

>gi|58032607|gb|AAW63086.1| anti-pneumococcal antibody 54B11 light chain [Homo sapiens]
Length=189

Score = 159 bits (403), Expect = 3e-38, Method: Composition-based stats.
Identities = 86/97 (88%), Positives = 87/97 (89%), Gaps = 0/97 (0%)

Query 6 QSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRSGS 65
QSPS LSASVGDRVTITCRASQGI N L WYQQKPGKAPK LIYAASTLQSGVPSRSGS
Sbjct 1 QSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASTLQSGVPSRSGS 60

Query 66 GSWTEFTLTISRLQPEDFATYYCQHQLNTYPWTFGQGT 102
GS TEFTLTIS LQPEDFATYYC N+YPWTFGQGT

Sbjct 61 GSGTEFTLTISLQPEDFATYYCLQHNSYPWTFGQGT 97

> gi|12655528|emb|CAC27615.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=103

Score = 159 bits (403), Expect = 3e-38, Method: Composition-based stats.
Identities = 91/100 (91%), Positives = 95/100 (95%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
++TQSPSFLSASVGDRVITCRASQGIS+YLAWSYQQKPGKAPKLLIYAASTLQSGVPSRF

Sbjct 2 QMTQSPSFLSASVGDRVITCRASQGISYYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 61

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
SGSGS TEFTLTIS LQPEDFATYYCQ LN+Y TFGQGT

Sbjct 62 SGSGSGTEFTLTISLQPEDFATYYCQQLNSYSITFGQGT 101

> gi|33355929|gb|AAQ16318.1| anti-human kappa light chain antibody Fab AbLBP1L [synthetic construct]

Length=239

Score = 159 bits (402), Expect = 4e-38, Method: Composition-based stats.
Identities = 84/101 (83%), Positives = 91/101 (90%), Gaps = 0/101 (0%)

Query 2 AELTQSPSFLSASVGDRVITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSR 61
AELTQSPS LSASVGDRV+ITCRASQ IS YL WYQQKPGKAPKLLIYAAS+L+SGVPSR

Sbjct 22 AELTQSPSSLSASVGDRVSIITCRASQTISRYLNWYQQKPGKAPKLLIYAASSLKSGVPSR 81

Query 62 FSGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102
FSGSGS T+FTLTIS LQPEDFATYYCQ N++P TFG GT

Sbjct 82 FSGSGSATDFTLTINSLQPEDFATYYCQQANSFPLTFGGGT 122

> gi|29725718|gb|AAO91639.1| U anti-HLA-A2/A28 immunoglobulin light chain variable region [Homo sapiens]

Length=107

Score = 159 bits (402), Expect = 4e-38, Method: Composition-based stats.
Identities = 86/99 (86%), Positives = 89/99 (89%), Gaps = 0/99 (0%)

Query 4 LTQSPSFLSASVGDRVITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 63
+TQSPSFL ASVGDRVITCRAS GISNY AWYQQKPGKAPKLLIYA STLQSGVPSRFS

Sbjct 4 MTQSPSFLXASVGDRVITCRASHGISNYFAWYQQKPGKAPKLLIYATSTLQSGVPSRFS 63

Query 64 GSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102

GSGS TEFTLTIS LQPEDFATYYCQ ++YP TFG GT

Sbjct 64 GSGSGTEFTLTISGLQPEDFATYYCQQYSSYPLTFGHGT 102

> gi|58222496|gb|AAW68880.1| U anti-tetanus toxoid immunoglobulin light chain variable region [Homo sapiens]

Length=107

Score = 159 bits (402), Expect = 4e-38, Method: Composition-based stats.
Identities = 86/99 (86%), Positives = 90/99 (90%), Gaps = 0/99 (0%)

Query 4 LTQSPSFLSASVGDRVITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRFS 63
+TQSP FLSASVGDRVITCRASQG+S YLAWSY Q KPGKAPKLLIYAASTLQSGVPSRFS

Sbjct 4 MTQSPPFLSASVGDRVITCRASQGLSTYLAWYQVKPGKAPKLLIYAASTLQSGVPSRFS 63

Query 64 GSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102

GSGS TEFTLTIS LQPEDFATYYCQ L+TYP T G GT

Sbjct 64 GSGSGTEFTLTINSLQPEDFATYYCQQLDTYPLTLGGGT 102

> gi|13171342|gb|AAK13633.1|AF234257_1 U immunoglobulin light chain variable region [Homo sapiens]
Length=107

Score = 159 bits (402), Expect = 4e-38, Method: Composition-based stats.
Identities = 85/100 (85%), Positives = 92/100 (92%), Gaps = 0/100 (0%)

Query 3 ELTQSPSFLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAASTLQSGVPSRF 62
E+TQSPS LSASVGDRVTITCRASQ I+N+LAWYQQ+PGKAP LLIY ASTLQ+GVPSRF

Sbjct 3 EMTQSPSTLSASVGDRVTITCRASQSINNWLAWYQQRPGKAPNLLIYKASTLQNGVPSRF 62

Query 63 SGSGSWTEFTLTISRLQPEDFATYYCQHLNTYPWTFGQGT 102

SGSGS TEFTLTIS LQP+DFATYYCQ N+YPWTFGQGT

Sbjct 63 SGSGSGTEFTLTISLQPDDFATYYCQQYNSYPWTFGQGT 102

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples

Posted date: Feb 26, 2007 5:55 PM

Number of letters in database: 1,607,774,624

Number of sequences in database: 4,657,147

Lambda K H
0.317 0.129 0.405

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 4657147

Number of Hits to DB: 32242863

Number of extensions: 1152658

Number of successful extensions: 2474

Number of sequences better than 10: 4

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 2503

Number of HSP's successfully gapped: 4

Length of query: 102

Length of database: 1607774624

Length adjustment: 71

Effective length of query: 31

Effective length of database: 1277117187

Effective search space: 39590632797

Effective search space used: 39590632797

T: 11

A: 40

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (20.4 bits)

S2: 71 (32.0 bits)

32

BLASTP 2.2.15 [Oct-15-2006]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference:

Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005.

RID: 1172616742-22831-88631162316.BLASTQ3

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples
4,657,147 sequences; 1,607,774,624 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

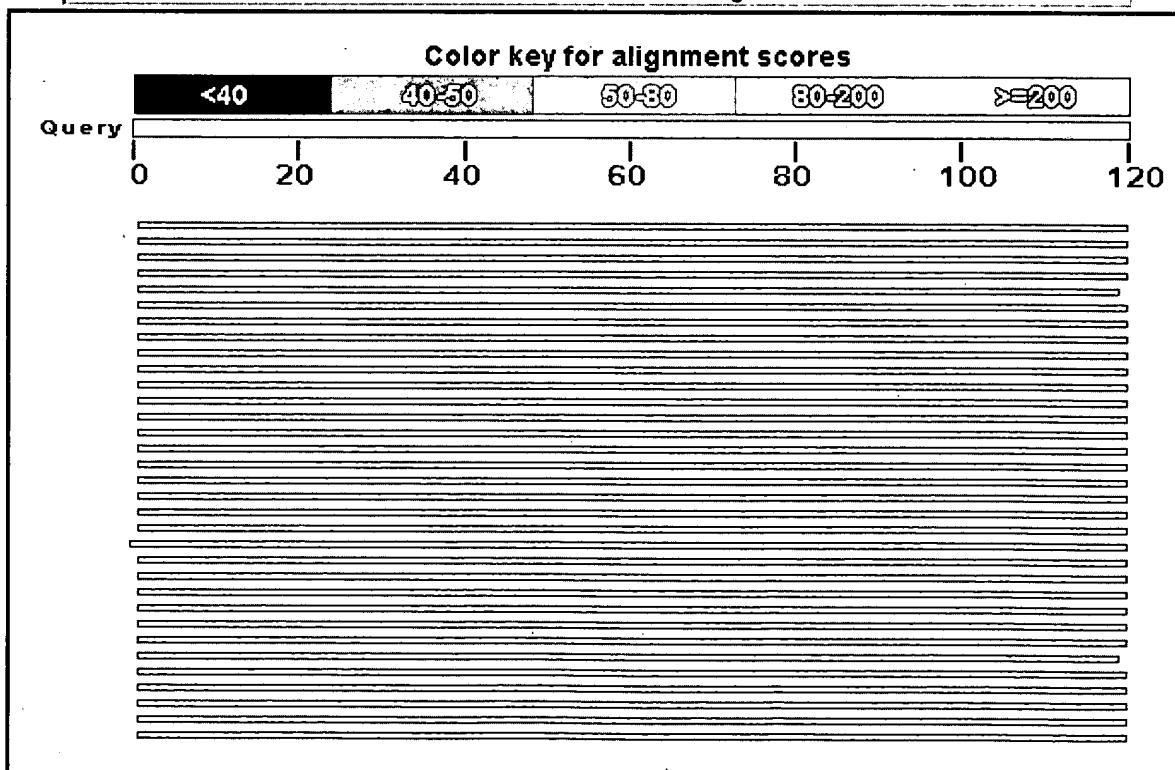
[Taxonomy reports](#)

Query= SEQ ID NO:7

Length=120

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments



Distance tree of results **NEW** Related Structures

Sequences producing significant alignments:

		Score (Bits)	E Value	
gi 9837148 gb AAG00448.1	anti-human melanoma single-chain va...	167	2e-40	
gi 87919 pir S14683	Ig mu chain precursor, membrane-bound (c...	166	3e-40	
gi 106898801 gb ABF83394.1	circulating B cell antibody heavy...	164	1e-39	U
gi 38382881 gb AAH62336.1	IGHG1 protein [Homo sapiens]	164	1e-39	UG
gi 15886932 emb CAC88723.1	immunoglobulin heavy chain variable	162	4e-39	U
gi 93279222 pdb 2DD8 H	Chain H, Crystal Structure Of Sars-Cov...	162	6e-39	S
gi 42543658 pdb 1RZI B	Chain B, Crystal Structure Of Human An...	160	3e-38	S
gi 87813 pir B32274	Ig heavy chain precursor V-I region (EVI...	159	3e-38	
gi 185151 gb AAA52828.1	immunoglobulin heavy chain precursor [H	159	3e-38	
gi 2344914 gb AAC51687.1	IgM heavy chain VH1 region precursor [159	4e-38	
gi 27728677 gb AAO17821.1	anti-rabies S057 immunoglobulin heavy	159	5e-38	U
gi 21668772 dbj BAC01413.1	immunoglobulin heavy chain VHDJ regi	159	5e-38	U
gi 3170859 gb AAC18234.1	immunoglobulin heavy chain variable re	158	7e-38	U
gi 122892236 gb ABM67185.1	immunoglobulin heavy chain variable	158	9e-38	
gi 118405991 gb ABK81358.1	immunoglobulin heavy chain variable	157	1e-37	
gi 45504721 gb AAS66904.1	immunoglobulin heavy chain variable r	157	1e-37	U
gi 45504713 gb AAS66900.1	immunoglobulin heavy chain variable r	157	1e-37	U
gi 2344944 gb AAC51702.1	IgM heavy chain VH1 region precursor [157	1e-37	
gi 29892991 emb CAD87747.1	immunoglobulin heavy chain variable	157	2e-37	U
gi 2344934 gb AAC51697.1	IgM heavy chain VH1 region precursor [157	2e-37	
gi 4468364 emb CAB38066.1	immunoglobulin heavy chain variable r	156	3e-37	U
gi 15886988 emb CAC88751.1	immunoglobulin heavy chain variable	156	3e-37	U
gi 118406380 gb ABK81550.1	immunoglobulin heavy chain variable	156	3e-37	
gi 21670665 dbj BAC02342.1	immunoglobulin heavy chain VHDJ regi	156	4e-37	U
gi 29892983 emb CAD87743.1	immunoglobulin heavy chain variable	155	4e-37	U
gi 106703 pir PH0958	Ig heavy chain V region (G6+ CLL-HUR) - hu	155	5e-37	
gi 20453025 gb AAM19761.1	immunoglobulin heavy chain variable r	155	5e-37	U
gi 15886946 emb CAC88730.1	immunoglobulin heavy chain variable	155	5e-37	U
gi 70798211 gb AAZ08818.1	immunoglobulin heavy chain variable r	155	5e-37	U
gi 15886958 emb CAC88736.1	immunoglobulin heavy chain variable	155	5e-37	U
gi 106897089 gb ABF83204.1	circulating B cell antibody heavy...	155	6e-37	U
gi 2344942 gb AAC51701.1	IgM heavy chain VH1 region precursor [155	6e-37	
gi 3170785 gb AAC18197.1	immunoglobulin heavy chain variable re	155	6e-37	U
gi 27261427 gb AAN85866.1	anti-keratin monoclonal antibody [...	155	6e-37	
gi 4456566 emb CAB37165.1	immunoglobulin heavy chain variable r	155	7e-37	U
gi 70798436 gb AAZ08930.1	immunoglobulin heavy chain variable r	155	7e-37	U

gi 15886984 emb CAC88749.1	immunoglobulin heavy chain variable	155	7e-37	U
gi 2344928 gb AAC51694.1	IgM heavy chain VH1 region precursor [155	8e-37	
gi 46255803 gb AAH69016.1	IGHG1 protein [Homo sapiens]	154	9e-37	UG
gi 3170841 gb AAC18225.1	immunoglobulin heavy chain variable re	154	1e-36	U
gi 1082511 pir S46394	Ig heavy chain V region - human >gi 13...	154	1e-36	
gi 45595687 gb AAH67091.1	IGHG1 protein [Homo sapiens]	154	1e-36	UG
gi 5679470 emb CAB51710.1	immunoglobulin heavy chain variable r	154	1e-36	U
gi 14573203 gb AAK67990.1	immunoglobulin heavy chain variable r	154	1e-36	U
gi 15886972 emb CAC88743.1	immunoglobulin heavy chain variable	154	1e-36	
gi 87239718 emb CAJ76653.1	anti-BINOL ScFv antibody [synthetic	154	1e-36	
gi 185325 gb AAB00782.1	Ig heavy chain	154	1e-36	
gi 106478 pir C33548	Ig heavy chain V-1 region (783) - human	154	2e-36	
gi 60616488 gb AAZ31272.1	immunoglobulin heavy chain variable r	154	2e-36	U
gi 106479 pir B33548	Ig heavy chain V-1 region (AND) - human	153	2e-36	
gi 46254144 gb AAS86042.1	immunoglobulin heavy chain [Homo sapi	153	2e-36	U
gi 70798229 gb AAZ08827.1	immunoglobulin heavy chain variable r	153	2e-36	U
gi 14573207 gb AAK67992.1	immunoglobulin heavy chain variabl...	153	2e-36	U
gi 45504715 gb AAS66901.1	immunoglobulin heavy chain variable r	153	2e-36	U
gi 70798404 gb AAZ08914.1	immunoglobulin heavy chain variable r	153	2e-36	U
gi 77158067 gb ABA62049.1	immunoglobulin epsilon heavy chain...	153	2e-36	
gi 74146792 gb ABA00058.1	immunoglobulin epsilon heavy chain...	153	2e-36	U
gi 58221628 gb AAW68456.1	anti-tetanus toxoid immunoglobulin...	153	2e-36	U
gi 3170813 gb AAC18211.1	immunoglobulin heavy chain variable re	153	2e-36	U
gi 39937969 gb AAR32404.1	immunoglobulin heavy chain variable r	153	3e-36	U
gi 4139210 gb AAD03728.1	immunoglobulin IgM heavy chain variabl	153	3e-36	U
gi 2344976 gb AAC51718.1	IgM heavy chain VH1 region precursor [153	3e-36	
gi 4836312 gb AAD30400.1 AF115114_1	immunoglobulin heavy chain v	153	3e-36	U
gi 225801 prf 1313976B	rheumatoid factor KAS	153	3e-36	
gi 10636975 emb CAC10771.1	immunoglobulin heavy chain variable	153	3e-36	
gi 21669729 dbj BAC01874.1	immunoglobulin heavy chain VHDJ regi	153	3e-36	U
gi 10444475 gb AAG17912.1	immunoglobulin heavy chain variable r	153	3e-36	
gi 21669963 dbj BAC01991.1	immunoglobulin heavy chain VHDJ regi	153	3e-36	U
gi 70798007 gb AAZ08716.1	immunoglobulin heavy chain variable r	152	3e-36	U
gi 3171039 gb AAC18320.1	immunoglobulin heavy chain variable re	152	3e-36	U
gi 3170697 gb AAC18153.1	immunoglobulin heavy chain variable re	152	3e-36	U
gi 3004730 gb AAC09104.1	IgM heavy chain variable region [Homo	152	3e-36	U
gi 58221859 gb AAW68566.1	anti-tetanus toxoid immunoglobulin...	152	4e-36	U
gi 115394132 gb ABI97021.1	anti-Burkholderia mallei scFv antibo	152	4e-36	
gi 21668738 dbj BAC01396.1	immunoglobulin heavy chain VHDJ regi	152	4e-36	U
gi 122892170 gb ABM67152.1	immunoglobulin heavy chain variable	152	4e-36	
gi 5679474 emb CAB51712.1	immunoglobulin heavy chain variable r	152	4e-36	U
gi 39939661 gb AAR32320.1	immunoglobulin heavy chain variable r	152	4e-36	U
gi 510402 emb CAA84416.1	IgM, variable region, rheumatoid fa...	152	4e-36	U
gi 744478 prf 2014394A	Ig, anti-thyroid peroxidase:SUBUNIT=heav	152	4e-36	
gi 37014261 gb AAQ87990.1	immunoglobulin E heavy chain variable	152	4e-36	
gi 20453027 gb AAM19762.1	immunoglobulin heavy chain variable r	152	4e-36	U
gi 45439530 gb AAS64360.1	immunoglobulin mu heavy chain variabl	152	4e-36	U
gi 20149023 gb AAM12759.1 AF492404_1	anti-human interleukin-2 sc	152	4e-36	
gi 40647142 gb AAR88377.1	anti-HIV-1 gp120 immunoglobulin 47e h	152	5e-36	U
gi 106701 pir PH0957	Ig heavy chain V region (G6+ CLL-BRA) - hu	152	5e-36	
gi 185302 gb AAB00779.1	Ig heavy chain	152	5e-36	
gi 34528319 dbj BAC85484.1	unnamed protein product [Homo sapien	152	5e-36	UG
gi 37693802 gb AAQ98912.1	immunoglobulin gamma light chain v...	152	5e-36	
gi 19848548 gb AAL17960.1	immunoglobulin heavy chain variable r	152	5e-36	U

gi 46254205 gb AAS86072.1	immunoglobulin heavy chain [Homo sapi	152	6e-36	U
gi 21669929 dbj BAC01974.1	immunoglobulin heavy chain VHDJ regi	152	6e-36	U
gi 7385061 gb AAF61676.1	immunoglobulin heavy chain variable re	152	6e-36	
gi 106480 pir A33548	Ig heavy chain V-1 region (NEI) - human	152	6e-36	
gi 118406366 gb ABK81543.1	immunoglobulin heavy chain variable	152	6e-36	
gi 39938343 gb AAR32589.1	immunoglobulin heavy chain variable r	152	6e-36	
gi 34595957 gb AAQ76696.1	immunoglobulin heavy chain variable r	152	7e-36	
gi 2344916 gb AAC51688.1	IgM heavy chain VH1 region precurs...	152	7e-36	
gi 70798055 gb AAZ08740.1	immunoglobulin heavy chain variable r	152	7e-36	U
gi 1498538 gb AAB06416.1	immunoglobulin heavy chain variable re	152	7e-36	U

Alignments

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> gi|9837148|gb|AAG00448.1| anti-human melanoma single-chain variable fragment antibody G71-1 immunoconjugate [synthetic construct]

Length=501

Score = 167 bits (422), Expect = 2e-40, Method: Composition-based stats.

Identities = 85/119 (71%), Positives = 93/119 (78%), Gaps = 9/119 (7%)

Query 2	LEQSGSEVKVPGSSLKVCKTSGGTFSTYTF	61
Sbjct 25	.V....A...K....V.....A.....S.AI.....	84

Query 62	FQDRVTITADESTSTVYMEVRRLRSED	120
Sbjct 85	..G.....K....A...LSS.....RGG-----	134

> gi|87919|pir||S14683 Ig mu chain precursor, membrane-bound (clone 201) - human
gi|33451|emb|CAA34971.1| **UG** unnamed protein product [Homo sapiens]

Length=627

Score = 166 bits (420), Expect = 3e-40, Method: Composition-based stats.
Identities = 87/124 (70%), Positives = 95/124 (76%), Gaps = 5/124 (4%)

Query 2	LEQSGSEVKVPGSSLKVCKTSGGTFSTYTF	61
Sbjct 23	.V....A...K....V.....A.....S.AI.....	82

Query 62	FQDRVTITADESTSTVYMEVRRLRSED	116
Sbjct 83	..G.....A...LSS.....GILGPYSSGWYPNSDYY.YG....	142

Query 117	GQGT	120
Sbjct 143	146

> gi|106898801|gb|ABF83394.1| **U** circulating B cell antibody heavy chain variable region [Homo sapiens]
Length=129

Score = 164 bits (415), Expect = 1e-39, Method: Composition-based stats.
Identities = 89/119 (74%), Positives = 98/119 (82%), Gaps = 1/119 (0%)

Query 2	LEQSGSEVKVPGSSLKVCKTSGGTFSTYTF	61
Sbjct 6	.V....A...K....V.....N.AI.....P.....I..F.T....QK	65

Query 62	FQDRVTITADESTSTVYMEVRRLRSED	120
Sbjct 66	..G.....D....A...MSS.....RDA.M-..I..VH..HDL....	123

> gi|38382881|gb|AAH62336.1| **UG**IGHG1 protein [Homo sapiens]

Length=470

Score = 164 bits (415), Expect = 1e-39, Method: Composition-based stats.
Identities = 86/119 (72%), Positives = 94/119 (78%), Gaps = 7/119 (5%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 23 .V...A...K....V.....V..M.....E.I.MF...E..QR 82

Query 62 FQDRVTITAESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVWGQGT 120
Sbjct 83N.A...LSS.....---SPAT.D.K...F.Y.... 134

> gi|15886932|emb|CAC88723.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=122

Score = 162 bits (411), Expect = 4e-39, Method: Composition-based stats.
Identities = 85/119 (71%), Positives = 94/119 (78%), Gaps = 1/119 (0%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V...A...K....V.....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTITAESTSTVYMEVRRRLRSEDTAVYYCAKT-SEVTATRGRTFFYSAMDVWGQG 119
Sbjct 64 ..G.....A...LSS.....RDPPDIVVVPA.IDY.YG..... 122

> gi|93279222|pdb|2DD8|H **S** Chain H, Crystal Structure Of Sars-Cov Spike Receptor-Binding Domain Complexed With Neutralizing Antibody

gi|93279898|pdb|2G75|A **S** Chain A, Crystal Structure Of Anti-Sars M396 Antibody
gi|93279900|pdb|2G75|C **S** Chain C, Crystal Structure Of Anti-Sars M396 Antibody

Length=245

Score = 162 bits (409), Expect = 6e-39, Method: Composition-based stats.
Identities = 86/119 (72%), Positives = 96/119 (80%), Gaps = 10/119 (8%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .Q...A...K....V.....A.....S..I.....L.....QK 63

Query 62 FQDRVTITAESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVWGQGT 120
Sbjct 64 ..G.....T.....A...LSS.....RDTVM----GG..... 112

> gi|42543658|pdb|1RZI|B **S** Chain B, Crystal Structure Of Human Anti-Hiv-1 Gp120-Reactive Antibody 47e Fab

gi|42543660|pdb|1RZI|D **S** Chain D, Crystal Structure Of Human Anti-Hiv-1 Gp120-Reactive Antibody 47e Fab

gi|42543662|pdb|1RZI|F **S** Chain F, Crystal Structure Of Human Anti-Hiv-1 Gp120-Reactive Antibody 47e Fab

gi|42543664|pdb|1RZI|H **S** Chain H, Crystal Structure Of Human Anti-Hiv-1 Gp120-Reactive Antibody 47e Fab

gi|42543666|pdb|1RZI|J **S** Chain J, Crystal Structure Of Human Anti-Hiv-1 Gp120-Reactive Antibody 47e Fab

gi|42543668|pdb|1RZI|L **S** Chain L, Crystal Structure Of Human Anti-Hiv-1 Gp120-Reactive Antibody 47e Fab

gi|42543670|pdb|1RZI|N **S** Chain N, Crystal Structure Of Human Anti-Hiv-1 Gp120-Reactive Antibody 47e Fab

gi|42543672|pdb|1RZI|P **S** Chain P, Crystal Structure Of Human Anti-Hiv-1 Gp120-Reactive Antibody 47e Fab

Length=230

Score = 160 bits (404), Expect = 3e-38, Method: Composition-based stats.
Identities = 85/120 (70%), Positives = 95/120 (79%), Gaps = 1/120 (0%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .L....A....K....V....A.....S.AI.....I.VF.S....QK 63

Query 62 FQDRVTITAESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYS-AMDVGQGT 120
Sbjct 64 ..G.....A...T...LSS.....F...GG.DGDYLSDP.Y.NHG..... 123

> gi|87813|pir||B32274 Ig heavy chain precursor V-I region (EVI-15) - human (fragment)
Length=135

Score = 159 bits (403), Expect = 3e-38, Method: Composition-based stats.
Identities = 82/123 (66%), Positives = 93/123 (75%), Gaps = 4/123 (3%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 7 .V....A...K....V....A.....S.A.....I.FL.TTH..QK 66

Query 62 FQDRVTITAESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATR---GRTFFYSAMDVG 117
Sbjct 67T....R.A...LHI.....I....RDQSLENIEVVPLDPNY..DG..... 126

Query 118 QGT 120
Sbjct 127 ... 129

> gi|185151|gb|AAA52828.1| immunoglobulin heavy chain precursor [Homo sapiens]
Length=136

Score = 159 bits (403), Expect = 3e-38, Method: Composition-based stats.
Identities = 82/123 (66%), Positives = 93/123 (75%), Gaps = 4/123 (3%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 7 .V....A...K....V....A.....S.A.....I.FL.TTH..QK 66

Query 62 FQDRVTITAESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATR---GRTFFYSAMDVG 117
Sbjct 67T....R.A...LHI.....I....RDQSLENIEVVPLDPNY..DG..... 126

Query 118 QGT 120
Sbjct 127 ... 129

> gi|2344914|gb|AAC51687.1| IgM heavy chain VH1 region precursor [Homo sapiens]
Length=148

Score = 159 bits (402), Expect = 4e-38, Method: Composition-based stats.
Identities = 85/120 (70%), Positives = 95/120 (79%), Gaps = 1/120 (0%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 23 .V....A...K....V....A.....S.AI.....I..F.T....QK 82

Query 62 FQDRVTITAESTSTVYMEVRRRLRSEDTAVYYCAK-TSEVTATRGRTFFYSAMDVGQGT 120
Sbjct 83 ..G.....A...LSS.....RDVPDIVVVAIYY.YG..... 142

> gi|27728677|gb|AAO17821.1| U anti-rabies S057 immunoglobulin heavy chain [Homo sapiens]
Length=476

Score = 159 bits (401), Expect = 5e-38, Method: Composition-based stats.
Identities = 81/120 (67%), Positives = 94/120 (78%), Gaps = 3/120 (2%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 23 .V....A...K....V....A.....NR..VN.....I..F.T....QR 82

Query 62 FQDRVTITAESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVGQGT 120
Sbjct 83 ..G.L.....A...LSS...D.....F..R--.NLDNS.TYYYF.GWF.P..... 140

> gi|21668772|dbj|BAC01413.1| **U** immunoglobulin heavy chain VHDJ region [Homo sapiens]
Length=125

Score = 159 bits (401), Expect = 5e-38, Method: Composition-based stats.
Identities = 87/119 (73%), Positives = 95/119 (79%), Gaps = 3/119 (2%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .Q...A...K....V.....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVGQGT 120
Sbjct 64 ..G.....A...LSS.....RDPG.AVAG---Y.YG..... 119

> gi|3170859|gb|AAC18234.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=147

Score = 158 bits (400), Expect = 7e-38, Method: Composition-based stats.
Identities = 88/119 (73%), Positives = 95/119 (79%), Gaps = 1/119 (0%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 23 .V...A...K....V.....A.....S.AI.....I..F.T....QK 82

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVGQGT 120
Sbjct 83 ..G.....A...LSS.....SFGSPA.IE..YYY.-G..... 140

> gi|122892236|gb|ABM67185.1| immunoglobulin heavy chain variable region [Homo sapiens]
Length=127

Score = 158 bits (399), Expect = 9e-38, Method: Composition-based stats.
Identities = 82/119 (68%), Positives = 96/119 (80%), Gaps = 3/119 (2%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 6 .VE..A...K....V.....A.....S.SIN.....I.MF.P....H. 65

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVGQGT 120
Sbjct 66 ..G.....R.A..DLSS...D.....RARVIL---A.YY.Y...A..... 121

> gi|118405991|gb|ABK81358.1| immunoglobulin heavy chain variable region [Homo sapiens]
Length=122

Score = 157 bits (398), Expect = 1e-37, Method: Composition-based stats.
Identities = 81/119 (68%), Positives = 90/119 (75%), Gaps = 0/119 (0%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V...A...K....V.....A..DIL.SFVI.....N..F.TP...QK 63

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVGQGT 120
Sbjct 64 ..G.....A...LSS.....RPQTTVT.PHHHYY.YG..... 122

> gi|45504721|gb|AAS66904.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=129

Score = 157 bits (398), Expect = 1e-37, Method: Composition-based stats.
Identities = 86/120 (71%), Positives = 96/120 (80%), Gaps = 1/120 (0%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V...A...K....V.....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSE-VTATRGRTFFYSAMDVGQGT 120

Sbjct 64 . . . G.....A...LSS.....RGADI.VVPAAMGYY.YG..... 123

> gi|45504713|gb|AAS66900.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=129

Score = 157 bits (398), Expect = 1e-37, Method: Composition-based stats.
Identities = 86/120 (71%), Positives = 96/120 (80%), Gaps = 1/120 (0%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V....A...K....V....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSE-VTATRGRTFFYSAMDVGQGT 120
Sbjct 64 ..G.....A...LSS.....RGGDI.VVPAAMSYY.YG..... 123

> gi|2344944|gb|AAC51702.1| IgM heavy chain VH1 region precursor [Homo sapiens]
Length=152

Score = 157 bits (397), Expect = 1e-37, Method: Composition-based stats.
Identities = 86/124 (69%), Positives = 95/124 (76%), Gaps = 5/124 (4%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 23 .V....A...K....V....A.....S.AI.....I..F.T....QK 82

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATR----GRTFFYSAMDVW 116
Sbjct 83 ..G.....A...LSS.....RDAAHNPP.EWQQQLDFNYY.YG.... 142

Query 117 GQGT 120
Sbjct 143 146

> gi|29892991|emb|CAD87747.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=130

Score = 157 bits (397), Expect = 2e-37, Method: Composition-based stats.
Identities = 86/120 (71%), Positives = 95/120 (79%), Gaps = 1/120 (0%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V....A...K....V....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSE-VTATRGRTFFYSAMDVGQGT 120
Sbjct 64 ..G.....A...LSS.....RGGDI.VVPAAMRYY.YG..... 123

> gi|2344934|gb|AAC51697.1| IgM heavy chain VH1 region precursor [Homo sapiens]
Length=146

Score = 157 bits (396), Expect = 2e-37, Method: Composition-based stats.
Identities = 87/119 (73%), Positives = 95/119 (79%), Gaps = 1/119 (0%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 23 .V....A...K....V....A.....S.AI.....I..F.T....QK 82

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVGQGT 120
Sbjct 83 ..G.....A...LSS.....R-.M.QGVINVLYY.YG.... 140

> gi|4468364|emb|CAB38066.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=118

Score = 156 bits (395), Expect = 3e-37, Method: Composition-based stats.
Identities = 87/120 (72%), Positives = 96/120 (80%), Gaps = 11/120 (9%)

Query 1 LLEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFSWVRQAPGQGLEWMGGITPIIGIANYAR 60
Sbjct 4A....K....V.....A.....S.AI.....R.I..L.....Q 63

Query 61 NFQDRVTTADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVGQGT 120
Sbjct 64 K..G.....K....A...LSS.....R----E...A----.I..... 112

> gi|15886988|emb|CAC88751.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=130

Score = 156 bits (395), Expect = 3e-37, Method: Composition-based stats.
Identities = 86/126 (68%), Positives = 95/126 (75%), Gaps = 7/126 (5%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFSWVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V....A...K....V.....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTTADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATR----GRTFFYSAMD 114
Sbjct 64 ..G.....A...LSS.....RDPPGQL.FLEWSILTKHYY.YG.. 123

Query 115 VWGQGT 120
Sbjct 124 129

> gi|118406380|gb|ABK81550.1| immunoglobulin heavy chain variable region [Homo sapiens]
Length=132

Score = 156 bits (394), Expect = 3e-37, Method: Composition-based stats.
Identities = 87/122 (71%), Positives = 95/122 (77%), Gaps = 4/122 (3%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFSWVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V....A...R....V.....A.....S.A.....L..FVTT...QK 63

Query 62 FQDRVTTADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRT---FFYSAMDVGQ 118
Sbjct 64 ..G.I..M.....T...LSS.....I....G-K.A..AE...DHLY.YG..... 122

Query 119 GT 120
Sbjct 123 .. 124

> gi|21670665|dbj|BAC02342.1| **U** immunoglobulin heavy chain VHDJ region [Homo sapiens]
Length=128

Score = 156 bits (394), Expect = 4e-37, Method: Composition-based stats.
Identities = 85/119 (71%), Positives = 93/119 (78%), Gaps = 0/119 (0%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFSWVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 ..L..AA...K....V.....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTTADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVGQGT 120
Sbjct 64 ..G.....A...LSS.....RDVYDIL.GYSLYY.YG..... 122

> gi|29892983|emb|CAD87743.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=125

Score = 155 bits (393), Expect = 4e-37, Method: Composition-based stats.
Identities = 86/121 (71%), Positives = 94/121 (77%), Gaps = 2/121 (1%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFSWVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V....A...K....V.....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTTADESTSTVYMEVRRRLRSEDTAVYYCAKT--SEVTATRGRTFFYSAMDVGQG 119
Sbjct 64 ..G.....A...LSS.....RVDGAM.QGVIPLGPY.YG..... 123

Query 120 T 120
Sbjct 124 . 124

>gi|106703|pir||PH0958 Ig heavy chain V region (G6+ CLL-HUR) - human (fragment)
Length=122

Score = 155 bits (392), Expect = 5e-37, Method: Composition-based stats.
Identities = 86/119 (72%), Positives = 92/119 (77%), Gaps = 6/119 (5%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFSWVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V....A....K....V....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVWGQGT 120
Sbjct 64 ..G.....A...LSS.....RVPN-----PL..AVG..... 116

>gi|20453025|gb|AAM19761.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=130

Score = 155 bits (392), Expect = 5e-37, Method: Composition-based stats.
Identities = 86/128 (67%), Positives = 94/128 (73%), Gaps = 9/128 (7%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFSWVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 1 .V....A....K....V....A.....S.AI.....I..F.T....QK 60

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKT-----SEVTATRGRTFFYSA 112
Sbjct 61 ..G.....A...LSS.....NNQGLLDYDFW.GYSHRLPGFY.YG 120

Query 113 MDVWGQGT 120
Sbjct 121 128

>gi|15886946|emb|CAC88730.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=124

Score = 155 bits (392), Expect = 5e-37, Method: Composition-based stats.
Identities = 85/121 (70%), Positives = 93/121 (76%), Gaps = 3/121 (2%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFSWVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V....A....K....V....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVT---ATRGRTFFYSAMDVWGQ 118
Sbjct 64 ..G.....A...LSS.....SPG.PNDFWSGSNYRYYY.YG..... 123

Query 119 G 119
Sbjct 124 . 124

>gi|70798211|gb|AAZ08818.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=126

Score = 155 bits (392), Expect = 5e-37, Method: Composition-based stats.
Identities = 85/119 (71%), Positives = 95/119 (79%), Gaps = 2/119 (1%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFSWVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V....A....K....V....A.....S..I.....I..F.T....QK 63

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVWGQGT 120
Sbjct 64 ..G.....A...LSS.....RE.TIFGV--VNWFVDF.I..... 120

>gi|15886958|emb|CAC88736.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=122

Score = 155 bits (392), Expect = 5e-37, Method: Composition-based stats.
Identities = 84/119 (70%), Positives = 92/119 (77%), Gaps = 0/119 (0%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V....A....K....V....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVWGQGT 120
Sbjct 64 ..G.....A...LSS.....RGGDYDYVW.SYRPND.F.I..... 122

>gi|106897089|gb|ABF83204.1| **U** circulating B cell antibody heavy chain variable region [Homo sapiens]
Length=127

Score = 155 bits (392), Expect = 6e-37, Method: Composition-based stats.
Identities = 86/119 (72%), Positives = 96/119 (80%), Gaps = 3/119 (2%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 6 .V....A....K....V....A.....S..I.....R.I..L.....QK 65

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVWGQGT 120
Sbjct 66 ..G.....K....A...LSS.....RDL...TFGPK---.NWF.P..... 121

>gi|2344942|gb|AAC51701.1| IgM heavy chain VH1 region precursor [Homo sapiens]
Length=141

Score = 155 bits (392), Expect = 6e-37, Method: Composition-based stats.
Identities = 86/119 (72%), Positives = 92/119 (77%), Gaps = 6/119 (5%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 23 .V....A....K....V....A.....S.AI.....I..F.T....QK 82

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVWGQGT 120
Sbjct 83 ..G.....A...LSS.....RVPN----PL..AVG..... 135

>gi|3170785|gb|AAC18197.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=146

Score = 155 bits (392), Expect = 6e-37, Method: Composition-based stats.
Identities = 85/119 (71%), Positives = 95/119 (79%), Gaps = 2/119 (1%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 23 .V....A....K....V....A.....S.AI.....I..F.T....QK 82

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVWGQGT 120
Sbjct 83 ..G.....K....A...LSS.....RGYDFVGSP.H--Y.YG..... 139

>gi|27261427|gb|AAN85866.1| anti-keratin monoclonal antibody [synthetic construct]
gi|30523031|gb|AAP31872.1| anti-keratin immunoglobulin heavy chain variable region [synthetic construct]
Length=123

Score = 155 bits (392), Expect = 6e-37, Method: Composition-based stats.
Identities = 85/120 (70%), Positives = 96/120 (80%), Gaps = 6/120 (5%)

Query 1 LLEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYAR 60
Sbjct 4A....K....V....A.....S.AI.....R.V..L.....Q 63

Query 61 NFQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVWGQGT 120
Sbjct 64 K..G.....K....A...LSS.....R----A.RHWVREASL..... 117

> gi|4456566|emb|CAB37165.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=127

Score = 155 bits (391), Expect = 7e-37, Method: Composition-based stats.
Identities = 85/119 (71%), Positives = 95/119 (79%), Gaps = 1/119 (0%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V....A...K....V.....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTITAESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVWGQGT 120
Sbjct 64 ..G.....A...LSS.....R-AM.RGVIHLDYY.YY.....K.. 121

> gi|70798436|gb|AAZ08930.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=122

Score = 155 bits (391), Expect = 7e-37, Method: Composition-based stats.
Identities = 85/119 (71%), Positives = 92/119 (77%), Gaps = 0/119 (0%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 1 .V....A...K....V.....A.....S.AI.....I..F.T....QK 60

Query 62 FQDRVTITAESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVWGQGT 120
Sbjct 61 ..G.....A...LSS.....VGRGYGNPATFYYY.YG..... 119

> gi|15886984|emb|CAC88749.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=125

Score = 155 bits (391), Expect = 7e-37, Method: Composition-based stats.
Identities = 85/121 (70%), Positives = 94/121 (77%), Gaps = 5/121 (4%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V....A...K....V.....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTITAESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTF--FYSAMDVWGQG 119
Sbjct 64 ..G.....A...LSS.....R--.PPS.NIVLMVYDD.F.I.... 120

Query 120 T 120
Sbjct 121 . 121

> gi|2344928|gb|AAC51694.1| IgM heavy chain VH1 region precursor [Homo sapiens]
Length=150

Score = 155 bits (391), Expect = 8e-37, Method: Composition-based stats.
Identities = 86/122 (70%), Positives = 96/122 (78%), Gaps = 3/122 (2%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 23 .V....A...K....V.....A.....S.AI.....I..F.T....QK 82

Query 62 FQDRVTITAESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRG---RTFFYSAMDVWGQ 118
Sbjct 83 ..G.....A...LSS.....RGTKGITIF.VVINYYYY.YG..... 142

Query 119 GT 120
Sbjct 143 .. 144

> gi|46255803|gb|AAH69016.1| **UG**IGHG1 protein [Homo sapiens]
Length=476

Score = 154 bits (390), Expect = 9e-37, Method: Composition-based stats.

Identities = 80/123 (65%), Positives = 92/123 (74%), Gaps = 9/123 (7%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSYTFSWVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 23 .V....A....K....V.....A.....D.PI.....I..F.AP...QK 82

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSA---MDVWG 117
Sbjct 83 ..G.....TE...N.A...LSS.....R----.P.NAFYYE.SGYLYF.L.. 137

Query 118 QGT 120
Sbjct 138 R.. 140

> gi|3170841|gb|AAC18225.1| Ig immunoglobulin heavy chain variable region [Homo sapiens]
Length=129

Score = 154 bits (390), Expect = 1e-36, Method: Composition-based stats.
Identities = 82/119 (68%), Positives = 93/119 (78%), Gaps = 0/119 (0%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSYTFSWVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V....A....K....V.....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDWGQGT 120
Sbjct 64 ..G.....K....A...LSS.....RQADCSGGSCYDI.PNWF.P.... 122

> gi|1082511|pir|IS46394 Ig heavy chain V region - human
gi|1335147|emb|CAA83486.1| Immunoglobulin heavy chain variable region (VH-50) [Homo sapiens]
Length=132

Score = 154 bits (390), Expect = 1e-36, Method: Composition-based stats.
Identities = 86/123 (69%), Positives = 95/123 (77%), Gaps = 4/123 (3%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSYTFSWVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V....A....K....V.....A.....S.AI.....I..F.T..H.QK 63

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRG---RTFFYSAMDWG 117
Sbjct 64 ..G.....A...LSS.....R.QLPA.DT.ILEWLPSY.YY.... 123

Query 118 QGT 120
Sbjct 124 K.. 126

> gi|45595687|gb|AAH67091.1| IgG IGHG1 protein [Homo sapiens]
Length=475

Score = 154 bits (390), Expect = 1e-36, Method: Composition-based stats.
Identities = 77/119 (64%), Positives = 89/119 (74%), Gaps = 2/119 (1%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSYTFSWVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 23 .V....A....K....V.....A..D..TN.AI.....I..F.TTD..Q. 82

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDWGQGT 120
Sbjct 83NLFSL.INN...K...M...VRE.FT.VFGVP.LH.--L.S.... 139

> gi|5679470|emb|CAB51710.1| Ig immunoglobulin heavy chain variable region [Homo sapiens]
Length=131

Score = 154 bits (389), Expect = 1e-36, Method: Composition-based stats.
Identities = 87/119 (73%), Positives = 95/119 (79%), Gaps = 1/119 (0%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSYTFSWVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V....A....K....V.....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVWGQGT 120
Sbjct 64 ..G.....A...LSS.....GPPD-..MVTLFYY.YG..... 121

> gi|14573203|gb|AAK67990.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=134

Score = 154 bits (389), Expect = 1e-36, Method: Composition-based stats.
Identities = 83/125 (66%), Positives = 96/125 (76%), Gaps = 5/125 (4%)

Query 1 LLEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFSWVRQAPGQGLEWMGGITPIIGIANYAR 60
Sbjct 4A...K....V.....A.....NKHAI.....R.ITMFDV....Q 63

Query 61 NFQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDV 115
Sbjct 64 K..G.....K....A...LSN.....RVERAAEAYYRSG.Y.YY..P... 123

Query 116 WGQGT 120
Sbjct 124 128

> gi|15886972|emb|CAC88743.1| **U** immunoglobulin heavy chain variable region [Homo sapiens]
Length=125

Score = 154 bits (389), Expect = 1e-36, Method: Composition-based stats.
Identities = 84/122 (68%), Positives = 93/122 (76%), Gaps = 3/122 (2%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFSWVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V...A...K....V.....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFF---YSAMDVWGQ 118
Sbjct 64 ..G.....A...LSS.....REAVRITIF.VVIIPRCT.F.I... 123

Query 119 GT 120
Sbjct 124 .. 125

> gi|87239718|emb|CAJ76653.1| anti-BINOL ScFv antibody [synthetic construct]
Length=249

Score = 154 bits (389), Expect = 1e-36, Method: Composition-based stats.
Identities = 85/119 (71%), Positives = 92/119 (77%), Gaps = 8/119 (6%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFSWVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V...A...K....V.....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVWGQGT 120
Sbjct 64 ..G.....A...LSS.....-----S..PYSDLK..... 114

> gi|185325|gb|AAB00782.1| Ig heavy chain
Length=146

Score = 154 bits (389), Expect = 1e-36, Method: Composition-based stats.
Identities = 86/119 (72%), Positives = 95/119 (79%), Gaps = 1/119 (0%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFSWVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 23 .V...A...K....V.....A.....S.AI.....I..F.T....QK 82

Query 62 FQDRVTITADESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVWGQGT 120
Sbjct 83 ..G.....A...LSS.....REV-.GCSSTSCYY.YG..... 140

> gi|106478|pir||C33548 Ig heavy chain V-1 region (783) - human
Length=133

Score = 154 bits (388), Expect = 2e-36, Method: Composition-based stats.
Identities = 87/124 (70%), Positives = 95/124 (76%), Gaps = 5/124 (4%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V....A....K....V.....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTITAESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRG----RTFFYSAMDVW 116
Sbjct 64 ..G.....A...LSS.....GILGPYSSGWYPNSDYY.YG.... 123

Query 117 GQGT 120
Sbjct 124 127

> gi|60616488|gb|AAX31272.1| U immunoglobulin heavy chain variable region [Homo sapiens]
Length=122

Score = 154 bits (388), Expect = 2e-36, Method: Composition-based stats.
Identities = 84/119 (70%), Positives = 93/119 (78%), Gaps = 2/119 (1%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V....A....K....V.....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTITAESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVGQGT 120
Sbjct 64 ..G.....A...LSS.....R--DPVDCS.GSCYL.WF.P.... 120

> gi|106479|pir||B33548 Ig heavy chain V-1 region (AND) - human
Length=126

Score = 153 bits (387), Expect = 2e-36, Method: Composition-based stats.
Identities = 85/119 (71%), Positives = 94/119 (78%), Gaps = 2/119 (1%)

Query 2 LEQSGSEVKVPGSSLKVSCCKTSGGTFSTYTFWSVRQAPGQGLEWMGGITPIIGIANYARN 61
Sbjct 4 .V....A....K....V.....A.....S.AI.....I..F.T....QK 63

Query 62 FQDRVTITAESTSTVYMEVRRRLRSEDTAVYYCAKTSEVTATRGRTFFYSAMDVGQGT 120
Sbjct 64 ..G.....A...LSS.....RV.IFGVV--QHYY.YY....L.. 120

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples

Posted date: Feb 26, 2007 5:55 PM

Number of letters in database: 1,607,774,624

Number of sequences in database: 4,657,147

Lambda K H
0.316 0.129 0.387

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 4657147

Number of Hits to DB: 37426471

Number of extensions: 1361095

Number of successful extensions: 3017

Number of sequences better than 10: 4

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 3064

Number of HSP's successfully gapped: 4

Length of query: 120

Length of database: 1607774624
Length adjustment: 87
Effective length of query: 33
Effective length of database: 1202602835
Effective search space: 39685893555
Effective search space used: 39685893555
T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (20.4 bits)
S2: 71 (32.0 bits)